

OIPF

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/727,628

DATE: 12/14/2000

TIME: 10:39:08

Input Set : A:\50597 rev SEQUENCE LISTING.txt

Output Set: N:\CRF3\12142000\I727628.raw

**ENTERED**

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3 <110> APPLICANT: Armstrong, Katherine
4   Hey, Timothy D
5   Folkerts, Otto
6   Smith, Kelley A
7   Hopkins, Nicole L
10 <120> TITLE OF INVENTION: MAIZE MIP SYNTHASE PROMOTER
12 <130> FILE REFERENCE: 50597
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/727,628
C--> 15 <141> CURRENT FILING DATE: 2000-12-01
17 <150> PRIOR APPLICATION NUMBER: US 60/168,612
18 <151> PRIOR FILING DATE: 1999-12-02
20 <160> NUMBER OF SEQ ID NOS: 3
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1959
26 <212> TYPE: DNA
27 <213> ORGANISM: Zea mays
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (137)..(1699)
33 <400> SEQUENCE: 1
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38 aggggaattaa ggcaag atg ttc atc gag agc ttc cgc gtc gag agc ccc cac 172
39   Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His
40       1           5           10
42 gtg cgg tac gcc cgg acg gag atc gag tcg gag tac cgg tac gac acg   220
43 Val Arg Tyr Gly Pro Thr Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr
44       15           20           25
46 acg gag ctg gty cac gag gcc aag gac gcc gcc tcc cgc tgg gtc gtc   268
47 Thr Glu Leu Val His Glu Ala Lys Asp Gly Ala Ser Arg Trp Val Val
48       30           35           40
50 cgc ccc aag tcc gtc aag tac aac ttc cgg acc agc acc gcc gtc ccc   316
51 Arg Pro Lys Ser Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro
52 45           50           55           60
54 aag ctc ggg gtc atg ctt gtg ggg tgg gga ggc aac aac ggg tcc acg   364
55 Lys Leu Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr
56       65           70           75
58 ctg acg gct ggg gtc att gcc aac agg gag ggg atc tca tgg gcg acc   412
59 Leu Thr Ala Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr
60       80           85           90
62 aag gac aag gty cag caa gcc aac tac tac gcc tcc ctc acc cag gct   460
63 Lys Asp Lys Val Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala
64       95          100          105
66 tcc acc atc aga gta gcc agc tac aac ggg gag gag ata tat gcg ccg   508
67 Ser Thr Ile Arg Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro
68      110          115          120

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70 ttc aag agc ctc cta ccc atg gtg aac cca gac gac ctt gtg ttt gga 556
71 Phe Lys Ser Leu Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly
72 125 130 135 140
74 ggc tgg gac atc agc agc atg aac ctg gca gat gcc atg acc agg gcc 604
75 Gly Trp Asp Ile Ser Ser Met Asn Leu Ala Asp Ala Met Thr Arg Ala
76 145 150 155
78 aag gtg ctg gac att gac ctg cag aag cag ctc agg ccc tac atg gag 652
79 Lys Val Leu Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu
80 160 165 170
82 tcc atg gtg cca ctt ccc ggt gtc tat gat ccg gac ttc atc gcc gct 700
83 Ser Met Val Pro Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala
84 175 180 185
86 aac cag ggc tct cgt gcc aac aat gtc atc aag gcc acc aag aaa gaa 748
87 Asn Gln Gly Ser Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu
88 190 195 200
90 cag gtg gag cag atc atc aaa gat atc agg gag ttt aag gag aag aac 796
91 Gln Val Glu Gln Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn
92 205 210 215 220
94 aaa gtg gac aag gta gtt gtg ctg tgg act gca aac act gaa agg tac 844
95 Lys Val Asp Lys Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr
96 225 230 235
98 agc aat gta tgt gct ggt ctc aac gac aca atg gag aat ctg ctg gca 892
99 Ser Asn Val Cys Ala Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala
100 240 245 250
102 tct gtg gac aag aac gag gcg gag atc tcg cca tca aca cta tat gcc 940
103 Ser Val Asp Lys Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala
104 255 260 265
106 att gcc tgt gtc acg gag ggg gtg ccg ttc atc aat ggg agc ccc cag 988
107 Ile Ala Cys Val Thr Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln
108 270 275 280
110 aac act ttt gtg cct ggg ctg att gat ctt gct atc aag aac aac tgc 1036
111 Asn Thr Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys
112 285 290 295 300
114 ctg atc ggt ggt gac gac ttc aag agt ggg cag acc aag atg aaa tcg 1084
115 Leu Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser
116 305 310 315
118 gtc ctg gtt gat ttt ctt gtt ggt gct gga ata aag ccc acc tcg att 1132
119 Val Leu Val Asp Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile
120 320 325 330
122 gtg agc tac aac cac ttg gga aac aac gac gcc atg aac ctg tct gcc 1180
123 Val Ser Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala
124 335 340 345
126 cct caa aca ttc agg tcc aag gag atc tcc aag agc aac gtg gtg gat 1228
127 Pro Gln Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp
128 350 355 360
130 gac atg gtc tca agc aat gcc att ctc tat ggg ccc gcc gag cat ccc 1276
131 Asp Met Val Ser Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro
132 365 370 375 380
134 gat cat gtt gtt gtc atc aag tat gtg ccg tat gtg gga gac agt aag 1324

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135 Asp His Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys
136          385          390          395
138 agg gct atg gac gag tac aca tca gag atc ttc atg ggc ggc aag agc 1372
139 Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser
140          400          405          410
142 acc atc gtg ctg cac aac acc tgc gag gac tcg ctc ctc gcc gca ccg 1420
143 Thr Ile Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro
144          415          420          425
146 atc atc ctc gat ctg gtg ctc ctg gct gag ctc agc acc agg atc cag 1468
147 Ile Ile Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln
148          430          435          440
150 tta aaa cct gag gga acg gac aag ttc cac tcc ttc cac ccg gtg gcc 1516
151 Leu Lys Pro Glu Gly Thr Asp Lys Phe His Ser Phe His Pro Val Ala
152 445          450          455          460
154 acc atc ctt agc tac ctc acc aag gca cca ctg gtt cca ccc ggc aca 1564
155 Thr Ile Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr
156          465          470          475
158 ccg gtg gtg aac gct ctt gca aag cag agg gcg atg ctg gag aac atc 1612
159 Pro Val Val Asn Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile
160          480          485          490
162 atg agg gct tgc gtt ggc ctg gcc cca gag aac aac atg atc ctg gag 1660
163 Met Arg Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu
164          495          500          505
166 tac aag tga gcy aag tgg cgt ggc ctg cag cta gat atg gaggaggctg 1709
167 Tyr Lys
168          510
170 cacgaagggg actagagagg cgagattagc tgtggaattg tgttggttc tcgtgttttc 1769
172 ttttgcgttc ttttctggt catcgctgtg gcgcttttgt attttatttg ttggaccgt 1829
174 aacctatca gggctctgct attagcgtt gaagcctgta atggcattgg catcgatatga 1889
176 taatgtgac gaggggtgcta gtccctaa aaaaaaaaaa aaaaaaac tcgagggggg 1949
178 gcccggtacc 1959
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182 <211> LENGTH: 510
183 <212> TYPE: PRT
184 <213> ORGANISM: Zea mays
186 <400> SEQUENCE: 2
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193 His Glu Ala Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
194 35 40 45
196 Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
197 50 55 60
199 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
200 65 70 75 80
202 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
203 85 90 95
205 Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg

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206          100          105          110
208 Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
209          115          120          125
211 Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
212          130          135          140
214 Ser Ser Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu Asp
215 145          150          155          160
217 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
218          165          170          175
220 Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
221          180          185          190
223 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
224          195          200          205
226 Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
227          210          215          220
229 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
230 225          230          235          240
232 Ala Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
233          245          250          255
235 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
236          260          265          270
238 Thr Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
239          275          280          285
241 Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
242          290          295          300
244 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
245 305          310          315          320
247 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
248          325          330          335
250 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
251          340          345          350
253 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
254          355          360          365
256 Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
257          370          375          380
259 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
260 385          390          395          400
262 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
263          405          410          415
265 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
266          420          425          430
268 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Pro Glu
269          435          440          445
271 Gly Thr Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
272          450          455          460
274 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
275 465          470          475          480
277 Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
278          485          490          495

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290 <400> SEQUENCE: 3
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295 acctatttat aacaacatc tgccaagaat acaattcttt tatacacaac ttatatgtga 180
297 gttctttttc tcttgttaact cttattaata aaacattttt ggctattaaa taatggcaac 240
299 taagttagca ccactgtaat tagattttgt ctggaacaat ttctctgact aagaagctat 300
301 ttggactctg cttttgccaa acaagtagaa aatgggaaccg ctcttataaa aaccattctc 360
303 acatcgctgg gtgctgaata aaactgaaaa cattagcttt ttatagctct cgctctctgc 420
305 tagtatgtgt tataaaatca ttttaccaat taccttttta aataactgta cgtagtttca 480
307 tcagttagaa tactcacgga gctaaaacaa aaaaagtgtg tctactgata aaagcagaga 540
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311 caaaacaaag ttgtattgta tggcctaaat tacagcacac tgacaccaca cgtatatatt 660
313 tctctctcca ttatcacagg atgtaactgt aaaaattttg tatgttaaac atttgtagta 720
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317 attttaataa aactgtaaat cgtctggctt cgtttctgga tggaggataa atagtgaata 840
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357 tctctcgcgc ggcgctcgct tacctcgcct cgcattccgt tcgagcaggg gagcggaagt 2040
359 gagaagggag ggaattaagg caaccatgg

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2069

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/727,628

DATE: 12/14/2000

TIME: 10:39:09

Input Set : A:\50597 rev SEQUENCE LISTING.txt

Output Set: N:\CRF3\12142000\I727628.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date